

SEQUENCE LISTING

<110> Schnorr, Kirk Matthew
Christensen, Lars Lehmann Hylling

<120> Fungal carbohydrate-binding module

<130> 10499.204-US

<160> 9

<170> PatentIn version 3.3

<210> 1

<211> 629

<212> DNA

<213> Pseudoplectania nigrella

 $\langle 220 \rangle$

<221> CDS

<222> (10) .. (531)

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Ile Gly Ala Ala Asn Ala His Thr Arg Val Tyr Gly Leu Ser Val Asn
15 20 25 30

gat gtc aca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc 147
Asp Val Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser
35 40 45

agt att gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt 195
 Ser Ile Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val
 50 55 60

cag gtc cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc 243
Gln Val Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr
65 70 75

gac atc cct act ttc act gct act gat gtt cct atc ttc acc aag aag 291
Asp Ile Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys
80 85 90

ccc caa cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct 339
Pro Gln Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser
95 100 105 110

gtt tca ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg 387
Val Ser Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala
115 120 125

agc aca atc ccg tca aaq ccc aaq act ccc qaa gag qtt aat aaq tgc 435

Ser Thr Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys
 130 135 140
 ctt gac gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga 483
 Leu Asp Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly
 145 150 155
 gga gtt gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat 531
 Gly Val Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
 160 165 170
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 gtaggggagg tgagatggag taagattaag cggccgca 629

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 35 40 45
 Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
 50 55 60
 Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
 65 70 75 80
 Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
 85 90 95
 Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
 100 105 110
 Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
 115 120 125
 Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
 130 135 140

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 145 150 155 160

Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
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<223> Positions 1-57 Candida lipase signal peptide, positions 58-147
Candida lipase sequence, positions 148-570 P. nigrella CBM
polypeptide.

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48

gtt gca gcc act cct ttg gtg aag tgc gca act agt ggc cat tac ggc
Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly
20 25 30

96

ctc gcg agg ccg cct cgg ccc caa cga att ctt gga ata tta agc ttt
Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe
35 40 45

144

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| tca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc agt att | 192 |
| Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile | |
| 50 55 60 | |
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| gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt cag gtc | 240 |
| Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val | |
| 65 70 75 80 | |
| | |
| cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc gac atc | 288 |
| Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile | |
| 85 90 95 | |
| | |
| cct act ttc act gct act gat gtt cct atc ttc acc aag aag ccc caa | 336 |
| Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln | |
| 100 105 110 | |
| | |
| cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct gtt tca | 384 |
| Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser | |
| 115 120 125 | |
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| ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg agc aca | 432 |
| Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr | |
| 130 135 140 | |
| | |
| atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc ctt gac | 480 |
| Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp | |
| 145 150 155 160 | |
| | |
| gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga gga gtt | 528 |
| Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val | |
| 165 170 175 | |
| | |
| gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat tag | 573 |
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| 180 185 190 | |

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<400> 9

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| Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly | |
| 20 25 30 | |
| | |
| Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe | |
| 35 40 45 | |

Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
50 55 60

Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
65 70 75 80

Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
85 90 95

Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
100 105 110

Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
115 120 125

Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
130 135 140

Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
145 150 155 160

Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
165 170 175

Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
180 185 190